

(TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Oct 6 04:39:24 1998; MasPar time 4667.32 Seconds
1514.879 Million cell updates/sec
Tabular output not generated.

Title: >US-08-908-884-1
Description: (3700-7548) from US08908884.seq (3 of 3)
Perfect Score: 3849
N.A. Sequence: 3700 GATGATATTGAGTTAGTCAA.....GGTGTGGCTAGTAGAAGCTT 7548
Comp: CTACTATAACTCAATCAGTT.....CCACACCGATCATCTTCGAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 532259 seqs, 918475165 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl55
1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro

Database: genbank107
12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat
18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st
24:gb_sts 25:gb_sy 26:gb_un 27:gb_vi

Statistics: Mean 12.169; Variance 5.411; scale 2.249

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description	Pred.	No.
			Match	Length	DB	ID			
	1	1949	50.6	5655	19	ATU87794	Arabidopsis thaliana t	0.00e+00	
	2	490	12.7	2104	19	ATU76707	Arabidopsis thaliana r	0.00e+00	
c	3	101	2.6	79837	19	AB005233	Arabidopsis thaliana g	2.69e-58	
c	4	92	2.4	7218	17	I66494	Sequence 14 from patent	1.44e-50	
c	5	52	1.4	7218	17	I66494	Sequence 14 from patent	5.55e-18	
c	6	39	1.0	10772	14	AF012089	Drosophila melanogaster	1.55e-08	
c	7	39	1.0	10772	14	AF012089	Drosophila melanogaster	1.55e-08	
c	8	31	0.8	215	17	I28278	Sequence 5 from patent	2.65e-03	
c	9	32	0.8	215	17	I28278	Sequence 5 from patent	6.36e-04	
c	10	31	0.8	354	14	OFU89259	Oxytricha fallax 57kD	2.65e-03	
c	11	28	0.7	354	14	OFU89259	Oxytricha fallax 57kD	1.64e-01	
c	12	26	0.7	370	14	OFU89262	Oxytricha fallax 57kD	2.20e+00	
c	13	26	0.7	448	24	G29607	human STS SHGC-33999,	2.20e+00	
c	14	26	0.7	37708	21	AC004034	Homo sapiens chromosom	2.20e+00	
c	15	26	0.7	48889	14	CEY57G11B	Caenorhabditis elegans	2.20e+00	
c	16	26	0.7	91017	21	HS162C6	Human DNA sequence fro	2.20e+00	
c	17	26	0.7	110384	21	HSAC000117	Human BAC clone RG062A	2.20e+00	
c	18	26	0.7	135672	21	HSAC000113	Human PAC clone DJ302C	2.20e+00	
c	19	27	0.7	194985	22	AC002406	Mouse chromosome X BAC	6.12e-01	
c	20	25	0.6	60	17	A34729	(modified) eglin N-ter	7.65e+00	
c	21	25	0.6	323	24	G10153	human STS CHLC.GATA101	7.65e+00	
c	22	24	0.6	354	14	AF036459	Trypanosoma cruzi muci	2.56e+01	
c	23	24	0.6	375	19	DEZ99136	Drimia elata chloropla	2.56e+01	
c	24	25	0.6	565	17	E04076	gDNA encoding envelope	7.65e+00	
c	25	25	0.6	882	27	HIVT1VI35	Human immunodeficiency	7.65e+00	
c	26	25	0.6	1659	17	E08319	cDNA encoding lucifera	7.65e+00	
c	27	24	0.6	1663	15	MVU92534	Mustela vison microsat	2.56e+01	
c	28	24	0.6	3853	16	CCNAKATP	C.commersoni mRNA for	2.56e+01	
c	29	25	0.6	3989	27	EPVSPHER	Entomopoxvirus gene fo	7.65e+00	
c	30	24	0.6	5656	21	HSU49957	Human LIM protein (LPP	2.56e+01	
c	31	24	0.6	6487	21	HSA2MGLB1	H.sapiens gene for alp	2.56e+01	
c	32	24	0.6	30758	13	CEH06I04	Caenorhabditis elegans	2.56e+01	
c	33	25	0.6	33274	14	CEF52B5	Caenorhabditis elegans	7.65e+00	
c	34	24	0.6	37738	14	CELF32B5	Caenorhabditis elegans	2.56e+01	
c	35	25	0.6	43589	14	CELC54D2	Caenorhabditis elegans	7.65e+00	
c	36	24	0.6	43637	14	CEB0399	Caenorhabditis elegans	2.56e+01	
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c	38	24	0.6	84510	19	AB006698	Arabidopsis thaliana g	2.56e+01	
c	39	24	0.6	112392	21	AC004028	Human PAC clone DJ0800	2.56e+01	
c	40	24	0.6	128598	12	D90912	Synechocystis sp. PCC6	2.56e+01	
c	41	24	0.6	130380	13	HS352E11	Human DNA sequence ***	2.56e+01	
c	42	24	0.6	132645	13	AC002345	*** SEQUENCING IN PROG	2.56e+01	
c	43	25	0.6	139698	13	HS929C8	Human DNA sequence ***	7.65e+00	
c	44	25	0.6	156399	21	AC002456	Human BAC clone RG013L	7.65e+00	
c	45	24	0.6	166983	21	AC002541	Human BAC clone RG043K	2.56e+01	

ALIGNMENTS

LOCUS ATU87794 5655 bp DNA PLN 25-MAY-1997
DEFINITION Arabidopsis thaliana transcription factor inhibitor I kappa B homolog (nim1) gene, complete cds.
ACCESSION U87794
NID g1916911
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; vascular plants; seed
plants; Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae;
Arabidopsis.
REFERENCE 1 (bases 1 to 5655)
AUTHORS Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,
Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and
Uknes,S.
TITLE The Arabidopsis NIM1 protein shows homology to the mammalian
transcription factor inhibitor I kappa B
JOURNAL Plant Cell 9 (3), 425-439 (1997)
MEDLINE 97246324
REFERENCE 2 (bases 1 to 5655)
AUTHORS Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,
Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and
Uknes,S.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1997) Fungicides, Novartis BGC, 3054 Cornwallis
Road, Research Triangle Park, NC 27709, USA
FEATURES Location/Qualifiers
source 1. .5655
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
/map="between ATHGENEA and nga111"
mRNA join(2754. .3347,3427. .4162,4271. .4474,4586. .5053)
gene 2787. .4866
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CDS join(2787. .3347,3427. .4162,4271. .4474,4586. .4866)
/gene="nim1"
/codon_start=1
/product="transcription factor inhibitor I kappa B
homolog"
/db_xref="PID:g1916912"
/translation="MDTTIDGFADSYEISSTSFVATDNTDSSIVYLAEQVLTGPDVS
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RPAVDFMLEVLYLAFIFKIPELITLYQRHLLDVVDKVVIEDTLVILKLANICGKACMK
LLDRCKEIVKSNVDMVSLEKSLPEELVKEIIDRRKELGLEVPKVKKHVSNVHKALDS
DDIELVKLLLKEDHTNLDDACALHFAVAYCNVKTATDLLKLDLADVNHRNPRGYTVLH
VAAMRKEPQLLISLLEKGASASEATLEGRTALMIAKQATMAECNNIPEQCKHSLKGR
LCVEILEQEDKREQIPRDVPPSFAVAADELKMTLLDLENRVALAQRLFPTEAQAAMEI
AEMKGTCEFIVTSLEPDRLTGTSPGVKIAPFRILEEHQSRLKALSKTVELGKRF
PRCSAVLDQIMNCEDLTQLACGEDDTAEKRLQKKQRYMEIQETLKKAFSEDNLELGNS
SLTDSTSSTSKSTGGKRSNRKLSHRRR"

BASE COUNT 1758 a 1014 c 1069 g 1814 t
ORIGIN

Query Match 50.6%; Score 1949; DB 19; Length 5655;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1961; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Db 3694 GATGATATTGAGTTAGTCAGTTGCTTTGAAAGAGGATCACACCAATCTAGATGATGCG 3753
Qy 3700 GATGATATTGAGTTAGTCAGTTGCTTTGAAAGAGGATCACACCAATCTAGATGATGCG 3759

Db 3754 TGTGCTCTCATTCGCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTAAAA 3813
Qy 3760 TGTGCTCTCATTCGCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTAAAA 3819

Db 3814 CTTGATCTGCCGATGTCAACCATAAGGAATCCGAGGGATATACGGTCTTCATGTTGCT 3873
Qy 3820 CTTGATCTGCCGATGTCAACCATAAGGAATCCGAGGGATATACGGTCTTCATGTTGCT 3879

Db 3874 GCGATGCGGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCA 3933
Qy 3880 GCGATGCGGAAGGAGCCACAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCA 3939

Db 3934 GAAGCAACTTGGAAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGTT 3993
Qy 3940 GAAGCAACTTGGAAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGTT 3999

Db 3994 GAATGTAATAATATCCGGAGCAATGCAAGCATTCTCTCAAAGGCCACTATGTGTAGAA 4053
Qy 4000 GAATGTAATAATATCCGGAGCAATGCAAGCATTCTCTCAAAGGCCACTATGTGTAGAA 4059

Db 4054 ATACTAGAGCAAGAAGACAAACGAGAACAAATTCTCTAGAGATGTTCTCCCTTTGCA 4113
Qy 4060 ATACTAGAGCAAGAAGACAAACGAGAACAAATTCTCTAGAGATGTTCTCCCTTTGCA 4119

Db 4114 GTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGGTATCTATCAA 4173
Qy 4120 GTGGCGGCCGATGAATTGAAGATGACGCTGCTCGATCTTGAAAATAGAGGTATCTATCAA 4179

Db 4174 GTCTTATTCTTATATGTTGAATTAAATTATGTCCTCTCTATTAGGAAACTGAGTGAA 4233
Qy 4180 GTCTTATTCTTATATGTTGAATTAAATTATGTCCTCTATTAGGAAACTGAGTGAA 4239

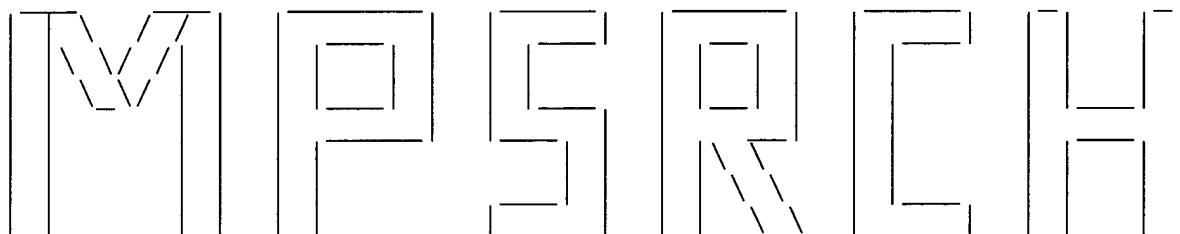
Db 4234 CTAATGATAACTATTCTTGTGTCGTCCACTGTTAGTTGCACCTGCTCAACGTCTTTT 4293
Qy 4240 CTAATGATAACTATTCTTGTGTCGTCCACTGTTAGTTGCACCTGCTCAACGTCTTTT 4299

Db 4294 CCAACGGAAGCACAAGCTGCAATGGAGATGCCGAAATGAAGGGAACATGTGAGTCATA 4353
Qy 4300 CCAACGGAAGCACAAGCTGCAATGGAGATGCCGAAATGAAGGGAACATGTGAGTCATA 4359

Db 4354 GTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGAGAACATCACC GG GTAAAG 4413
Qy 4360 GTGACTAGCCTCGAGCCTGACCGTCTCACTGGTACGAAGAGAACATCACC GG GTAAAG 4419

Db 4414 ATAGCACCTTCAGAACCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTCTAAAACC 4473
Qy 4420 ATAGCACCTTCAGAACCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTCTAAAACC 4479
Db 4474 GGTATGGATTCTCACCCACTTCATCGGACTCCTTATCACAAAAACAAAACCTAAATGATC 4533
Qy 4480 GGTATGGATTCTCACCCACTTCATCGGACTCCTTATCACAAAAACAAAACCTAAATGATC 4539
Db 4534 TTTAACATGGTTTGTACTTGCTGTCGACCTGTTTTTATCATCAGTGGAACTC 4593
Qy 4540 TTTAACATGGTTTGTACTTGCTGTCGACCTGTTTTT-ATCATCAGTGGAACTC 4598
Db 4594 GGGAAACGATTCTCCCGCGCTTCCCGCAGTGCTCGACCAGATTATGAACGTGAGGAC 4653
Qy 4599 GGGAAACGATTCTCCCGCGCTTCCCGCAGTGCTCGACCAGATTATGAACGTGAGGAC 4658
Db 4654 TTGACTCAACTGGCTTGCAGAGACGACACTGCTGA-GAAACGACTACAAAAGAAGCA 4712
Qy 4659 TTGACTCAACTGGCTTGCAGAGACGACACTGCTGAAGAACGACTACAAAAGAAGCA 4718
Db 4713 AAGGTACATGGAAATAAAGAGACACTAAAGAACGGCTTACTGTGAGGACAATTGGAATT 4772
Qy 4719 AAGGTACATGGAAATAAAGAGACACTAAAGAACGGCTTACTGTGAGGACAATTGGAATT 4778
Db 4773 AGGAAATTCTGCCCTGACAGATTGACTCTTCCACATCGAAATCAACCGGTGGAAAGAG 4832
Qy 4779 AGGAAATTCTGCCCTGACAGATTGACTCTTCCACATCGAAATCAACCGGTGGAAAGAG 4838
Db 4833 GTCTAACCGTAAACTCTCATCGTCGTCGGTGAGACTCTGCCTCTTAGTGTAAATT 4892
Qy 4839 GTCTAACCGTAAACTCTCATCGTCGTCGGTGAGACTCTGCCTCTTAGTGTAAATT 4898
Db 4893 GCTGTACCATATAATTCTGTTTCAATGACTGTAACGTGTTATGTCTATCGTGGCGT 4952
Qy 4899 GCTGTACCATATAATTCTGTTTCAATGACTGTAACGTGTTATGTCTATCGTGGCGT 4958
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Qy 4959 CATATAGTTCGCTTCGTTGCATCCTGTGTATTATTGCTGCAGGTGTGCTCAAAC 5018
Db 5013 AAATGTTGTAACAATTGAACCAATGGTATACAGATTGTAATATATATTGTACATC 5072
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Db 5073 AACAAATAACCCATGATGGTGTACAGAGTTGCTAGAATCAAAGTGTGAAATAATGTCAA 5132
Qy 5079 AACAAATAACCCATGATGGTGTACAGAGTTGCTAGAATCAAAGTGTGAAATAATGTCAA 5138
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Qy 5139 TTGTTCATCTGTTGGATATTCCACCAAGAACCAAAAAGAATATTCAAGTCCCTGAACT 5198
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Qy 5559 CCACTGATTTGAGGGAATTGGGCTAACCATTCGAGCTCTGAGTCCTTCTTTTGAT 5618
Db 5613 GTCCTTATGTAGGAATCAAATTCTCCTCTGACTTGTGGAT 5655
Qy 5619 GTCCTTATGTAGGAATCAAATTCTCCTCTGACTTGTGGAT 5661



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Oct 6 07:04:53 1998; MasPar time 555.70 Seconds
942.362 Million cell updates/sec

Tabular output not generated.

Title: >US-08-908-884-1
Description: (3700-7548) from US08908884.seq (3 of 3)
Perfect Score: 3849
N.A. Sequence: 3700 GATGATATTGAGTTAGTCAA..... GGTGTGGCTAGTAGAAGCTT 7548
Comp: CTACTATAACTCAATCAGTT..... CCACACCGATCATCTTCGAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq32
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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 10.057; Variance 5.467; scale 1.840

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description	Pred. No.
	No.	Score	Match	Length	DB	ID		
c	1	2827	73.4	9919	40	V04631	Arabidopsis thaliana	0.00e+00
	2	1949	50.6	5655	40	V04632	Arabidopsis thaliana	0.00e+00
	3	49	1.3	204	1	N81164	Base substituted E.co	3.60e-15
	4	41	1.1	91	9	Q51746	Oligonucleotide probe	4.11e-10
c	5	42	1.1	91	9	Q51746	Oligonucleotide probe	9.88e-11
c	6	40	1.0	204	1	N81164	Base substituted E.co	1.69e-09
	7	33	0.9	114	12	Q70465	Generic DNA sequence	2.44e-05
c	8	34	0.9	114	12	Q70467	Generic DNA sequence	6.45e-06
c	9	29	0.8	67	24	T14322	Primer used in the la	4.20e-03
	10	32	0.8	114	12	Q70467	Generic DNA sequence	9.05e-05
	11	30	0.8	114	12	Q70468	Generic DNA sequence	1.19e-03
	12	30	0.8	114	12	Q70469	Generic DNA sequence	1.19e-03
	13	29	0.8	114	12	Q70466	Generic DNA sequence	4.20e-03
c	14	32	0.8	114	12	Q70465	Generic DNA sequence	9.05e-05
c	15	32	0.8	114	12	Q70468	Generic DNA sequence	9.05e-05
c	16	31	0.8	114	12	Q70470	Generic DNA sequence	3.31e-04
c	17	31	0.8	114	12	Q70469	Generic DNA sequence	3.31e-04
c	18	30	0.8	114	12	Q70466	Generic DNA sequence	1.19e-03
c	19	29	0.8	114	12	Q70473	Generic DNA sequence	4.20e-03
c	20	31	0.8	178	32	T76405	Human endothelin-1 an	3.31e-04
	21	28	0.7	39	7	Q51787	Mixed oligonucleotide	1.46e-02
	22	28	0.7	114	12	Q70472	Generic DNA sequence	1.46e-02
	23	28	0.7	114	12	Q70470	Generic DNA sequence	1.46e-02
	24	27	0.7	114	12	Q70473	Generic DNA sequence	4.93e-02
	25	26	0.7	114	12	Q70471	Generic DNA sequence	1.64e-01
c	26	27	0.7	114	12	Q70472	Generic DNA sequence	4.93e-02

C	27	26	0.7	168	32	T76270	Human MDNCF antisense	1.64e-01
	28	26	0.7	178	32	T76405	Human endothelin-1 an	1.64e-01
	29	28	0.7	250	32	T76438	Substance P antisense	1.46e-02
	30	27	0.7	501	3	N50028	Sequence encoding new	4.93e-02
	31	27	0.7	501	3	N50033	Sequence encoding new	4.93e-02
	32	27	0.7	501	3	N50027	Sequence encoding new	4.93e-02
	33	26	0.7	501	3	N50029	Sequence encoding new	1.64e-01
C	34	26	0.7	501	3	N50030	Sequence encoding new	1.64e-01
	35	26	0.7	984	17	Q94336	Degenerate Alteromon	1.64e-01
C	36	25	0.6	82	21	T13610	DC43 TSAR library gen	5.29e-01
	37	25	0.6	498	3	N50034	Sequence encoding new	5.29e-01
	38	25	0.6	501	3	N50024	Sequence encoding new	5.29e-01
	39	25	0.6	501	3	N50032	Sequence encoding new	5.29e-01
	40	25	0.6	501	3	N50031	Sequence encoding new	5.29e-01
C	41	25	0.6	501	3	N50026	Sequence encoding new	5.29e-01
C	42	25	0.6	501	3	N50025	Sequence encoding new	5.29e-01
C	43	25	0.6	501	3	N50032	Sequence encoding new	5.29e-01
C	44	25	0.6	501	3	N50023	Sequence encoding new	5.29e-01
C	45	25	0.6	501	3	N50029	Sequence encoding new	5.29e-01

ALIGNMENTS

RESULT 1

ID V04631 standard; DNA; 9919 BP.

AC V04631;

DT 17-JUN-1998 (first entry)

DE Arabidopsis thaliana BAC-04 containing the NIM1 gene.

KW NIM1; noninducible immunity; disease resistance; plants;

KW SAR gene expression; ss.

OS Arabidopsis thaliana.

PN WO9749822-A1.

PD 31-DEC-1997.

PF 10-MAR-1997; E01218.

PR 10-JAN-1997; US-035022.

PR 21-JUN-1996; US-020272.

PR 30-AUG-1996; US-024883.

PR 13-DEC-1996; US-033177.

PR 27-DEC-1996; US-773559.

PA (NOVS) NOVARTIS AG.

PI Delaney TP, Ellis DM, Friedrich LB, Johnson JE,

PI Lawton KA, Ryals JA, Weymann K;

DR WPI; 98-077185/07.

PT NIM1 gene which allows activation in plant of systemic acquired

PT resistance - useful to confer broad spectrum disease resistance in

PT plants, specifically crop plants, e.g. rice, wheat, barley, rye and

PT corn

PS Claim 4; Fig 14; 153pp; English.

CC The sequence is that of the 9.9kb region of clone BAC-04 containing

CC the NIM1 (noninducible immunity) gene. It may be used to confer a

CC broad spectrum disease resistance in plants, specifically crop plants,

CC e.g. rice, wheat, barley, rye and corn. The NIM1 gene can be used to

CC confer universal disease susceptibility to plant cells, and their

CC progeny. It can also be used in a screening method for identifying

CC compounds capable of inducing broad spectrum disease resistance in
CC plants, while the plant cells, and their progeny, can be used to
CC isolate a gene fragment which allows expression of broad spectrum
CC disease resistance in plants, or to incorporate the resistant trait
CC into plant lines through breeding.

SQ Sequence 9919 BP; 3150 A; 1826 C; 1737 G; 3206 T;

Query Match 73.4%; Score 2827; DB 40; Length 9919;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 2864; Conservative 0; Mismatches 1; Indels 6; Gaps 6;

Db	1	tgtatcatgaattgcgttagggtgtttaaagataaggatgagctgaagaaggcggt	60
Cp	6567	TGATCATGAATTGCCTGTAGGGTTGTGTTAAAGATAGGGATGAGCTGAAGAAGGCCTG	6508
Db	61	ggactgggttccattagagggcagcaaaagtgttagtacaagagattgagaaggacga	120
Cp	6507	GGACTGGTGTCCATTAGAGGGCAGCAAAAGTGTAGTACAAGAGATTGAGAAGGACGA	6448
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Cp	6087	TGAATTTCATCCTCGGTGGCGCGTTGGCGTTCCACAGTCCATTGAAGGGTTCA	6028
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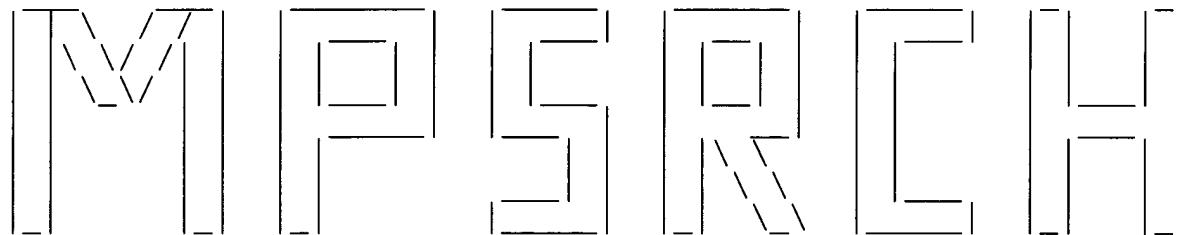
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Cp 4350 ACATGTTCCCTTCATTGCGCATCTCCATTGCAGCTTGTGCTCCGTTGGAAAAAGACG 4291

RESULT 2
ID V04632 standard; DNA; 5655 BP.
AC V04632;
DT 17-JUN-1998 (first entry)
DE *Arabidopsis thaliana* NIM1 gene.
KW NIM1; noninducible immunity; disease resistance; plants;
KW SAR gene expression; ss.
OS *Arabidopsis thaliana*.
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= "NIM1 protein"
FT exon 2787..3347

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Qy 3880 GCGATGCGGAAGGAGCCACAATTGATACTATCTTATTGGAAAAAGGTGCAAGTGCATCA 3939
Db 3934 gaagcaacttggaaaggtagaaccgcactcatgatcgcaaaacaagccactatggcggtt 3993
Qy 3940 GAAGCAACTTGGAAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTT 3999
Db 3994 gaatgtataatatccggagcaatgcaagcattctctcaaaggccactatgtgtagaa 4053
Qy 4000 GAATGTAATAATATCCGGAGCAATGCAAGCATTCTCTCAAAGGCCACTATGTGTAGAA 4059
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Qy 4060 ATACTAGAGCAAGAAGACAAACGAGAACAAATTCTAGAGATGTTCCCTCCCTTTGCA 4119
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Qy	5619	GTCCTTATGTAGGAATCAAATTCTCCCTCTGACTGTGGAT	5661



(TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Oct 6 05:58:05 1998; MasPar time 3957.16 Seconds
1362.257 Million cell updates/sec
Tabular output not generated.

Title: >US-08-908-884-1
Description: (3700-7548) from US08908884.seq (3 of 3)
Perfect Score: 3849
N.A. Sequence: 3700 GATGATATTGAGTTAGTCAA..... GGTGTGGCTAGTAGAAGCTT 7548
Comp: CTACTATAACTCAATCAGTT..... CCACACCGATCATCTCGAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1832099 seqs, 700269816 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est55

Database:	1:em_est10 2:em_est11 genbank-est107 3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13 8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17 12:gb_est18 13:gb_est19 14:gb_est2 15:gb_est20 16:gb_est21 17:gb_est22 18:gb_est23 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6 23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss						
Statistics:	Mean 12.357; Variance 2.094; scale 5.901						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result	Query	%					
No.	Score	Match	Length	DB	ID	Description	Pred. No.

c 1	377	9.8	470	11	AA395706	28108 Lambda-PRL2 Arab	0.00e+00
c 2	276	7.2	798	26	B21790	F7A9-Sp6 IGF Arabidops	0.00e+00
c 3	235	6.1	258	11	T22612	4620 Lambda-PRL2 Arabi	0.00e+00
c 4	208	5.4	909	26	B13248	F21L17-Sp6 IGF Arabido	0.00e+00
c 5	154	4.0	783	26	B20373	F7D16-Sp6 IGF Arabidop	1.12e-279
c 6	155	4.0	868	26	B20379	F7O9-Sp6 IGF Arabidops	4.86e-282
c 7	154	4.0	936	26	B11275	F11H8-T7 IGF Arabidops	1.12e-279
c 8	150	3.9	785	26	B20920	F22C12-T7 IGF Arabidop	3.01e-270
c 9	77	2.0	629	26	B26306	F18D8TF IGF Arabidopsi	6.04e-104
c 10	71	1.8	252	13	AA754459	97SN1787 Rice Immature	4.28e-91
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c 12	51	1.3	247	13	AA754458	97SN1784 Rice Immature	3.91e-50
c 13	47	1.2	247	13	AA754458	97SN1784 Rice Immature	2.01e-42
c 14	40	1.0	2275	12	AF034173	Homo sapiens ntcon2 co	1.71e-29
c 15	34	0.9	448	26	B24539	F20L24TF IGF Arabidops	3.71e-19
c 16	35	0.9	2275	12	AF034173	Homo sapiens ntcon2 co	8.04e-21
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c 19	26	0.7	619	26	FR0004306	F.rubripes GSS sequenc	5.93e-07
c 20	24	0.6	153	8	AA566154	MA3AS043.AAS S. manson	2.69e-04
c 21	23	0.6	214	6	HUM003B01A	Human fetal brain cDNA	4.81e-03
c 22	24	0.6	309	21	ATTS1721	A. thaliana transcribe	2.69e-04
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c 34	23	0.6	452	7	AA447498	zw90h04.r1 Soares tota	4.81e-03

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36	24	0.6	481	17	C83144	Oryctolagus cuniculus	Oryctolagus cuniculus	2.69e-04	
c	37	24	0.6	481	17	C83011	Oryctolagus cuniculus	2.69e-04	
	38	24	0.6	491	20	N28331	yx26a03.r1	Homo sapien	2.69e-04
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ALIGNMENTS

RESULT 1

LOCUS AA395706 470 bp mRNA EST 31-OCT-1997

DEFINITION 28108 Lambda-PRL2 *Arabidopsis thaliana* cDNA clone 9905XP 3', mRNA sequence.

ACCESSION AA395706

NID g2048931

KEYWORDS EST.

SOURCE thale cress.

ORGANISM *Arabidopsis thaliana*
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 470)

AUTHORS Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.

TITLE Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous *Arabidopsis* cDNA clones

JOURNAL Plant Physiol. 106, 1241-1255 (1994)

MEDLINE 95148729

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Lansing, Mi
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: M13 -21 dye primer.

FEATURES Location/Qualifiers

source 1. .470
/organism="Arabidopsis thaliana"
/strain="var columbia"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light

cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

/db_xref="taxon:3702"
/clone="9905XP"
/clone_lib="Lambda-PRL2"

BASE COUNT 119 a 101 c 99 g 143 t 8 others
ORIGIN

Query Match 9.8%; Score 377; DB 11; Length 470;
Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 409; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

Db 49 CTCAACTGGCTTCCGGAGAGGNCACCCCTGCTGG-GAACCGNCTACCAAAGGAAGCAAAG 107
Qy 4663 CTCAACTGGCTTGCAGAGACACTGCTGAAGAACGACTACAAAAG-AAGCAAAG 4721
Db 108 GTCCATGGAA-TACAAGAGNCACTAAAGAACGGCTTACTGAGGACAATTGGAATTAGG 166
Qy 4722 GTACATGGAAATACAAGAGACACTAAAGAACGGCTTACTGAGGACAATTGGAATTAGG 4781
Db 167 AAATTCTGCCCTGACAGATTGACTTCTCCCACATCGAAATCAACCGGTGGAAAGAGGT 226
Qy 4782 AAATTCTGCCCTGACAGATTGACTTCTTCC-ACATCGAAATCAACCGGTGGAAAGAGGT 4840
Db 227 CTAACCGTAAACTCTCATCGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAAATTTC 286
Qy 4841 CTAACCGTAAACTCTCATCGTCGTCGGTGAGACTCTTGCCTCTTAGTGTAAATTTC 4900
Db 287 TGTACCATATAATTCTGTTTCAATGATGACTGTAACGTGTTATGCTATCGTTGGCGTCA 346
Qy 4901 TGTACCATATAATTCTGTTTCAATGATGACTGTAACGTGTTATGCTATCGTTGGCGTCA 4960
Db 347 CATAGTTCGCTCTCGTTGCATCCTGTATTGCTGCAGGTGTGCTCAAACAA 406
Qy 4961 TATAGTTCGCTCTCGTTGCATCCTGTATTGCTGCAGGTGTGCTCAAACAA 5020
Db 407 ATGTTGTAACAATTGAACCAATGGTATACAGATTGTAATATATATTATGTACATCAA 466
Qy 5021 ATGTTGTAACAATTGAACCAATGGTATACAGATTGTAATATATATTATGTACATCAA 5080
Db 467 CAAT 470
Qy 5081 CAAT 5084